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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS AND APPARATUS FOR GENETIC EVALUATION

(57) Abstract: Rapid and definitive bioagent detection and identification can be carried out without nucleic acid sequencing. Analysis of a variety of bioagents and samples, such as air, fluid, and body samples, can be carried out to provide information useful for industrial, medical, and environmental purposes. Nucleic acid samples of unknown or suspected bioagents may be collected, optimal primer pairs may be selected, and the nucleic acid may be amplified. Expected mass spectra signal models may be generated and selected, the actual mass spectra of the amplicons may be obtained. The expected mass spectra most closely correlating with the actual mass spectra may be determined using a joint maximum likelihood analysis, and base counts for the actual mass spectra and the expected mass spectra may be obtained. The most likely candidate bioagents may then be determined.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/11877

A. CLASSIFICATION OF SUBJECT MATTER
IPC: **C12Q 1/68**(2006.01);**G01N 33/48**(2006.01)

USPC: 435/6;702/19,20
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/6; 702/19,20

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN and EAST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LEWERS et al. Detection of Linked QTL for Soybean Brown Stem Rot Resistance in 'BSR 101' as Expressed in a Growth Chamber Environment. Molecular Breeding. 1999, Vol. 5, pages 33-42, especially pages 33-36.	1-9
A	PATERSON et al. Fine Mapping of Quantitative Trait Loci Using Selected Overlapping Recombinant Chromosomes, in an Interspecies Cross of Tomato. Genertics. March 1990, Vol. 124, pages 735-742, especially pages 735-737.	1-9
A	JIANG et al. Multiple Traint Analysis of Genetic Mapping for Quantitative Trait Loci. Genetics. 1995, Vol. 140, pages 1111-1127, especially pages 1111-1121.	1-9
A	ZENG, Z.-B. Precision Mapping of Quantitative Trait Loci. Genetics. April 1994, Vol. 136, pages 1457-1468, especially pages 1457-1463.	1-9

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/11877

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	JANSEN et al. Genotype-by-environment Interaction in Genetic Mapping of Multiple Quantitative Trait Loci. Theor. Appl. Genet. 1995, Vol. 91, pages 33-37, especially pages 33-35.	1-9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/11877

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of any additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
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BOX III. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I (claims 1-9), drawn to a method of automating the determination of a distinguishing genotypic sequence for a member

Group II (claims 10-17), drawn to a method of determining computationally in a non-linear manner a number of primer sets.

Group III (claims 18-26), drawn to a method of determining computationally in a non-linear manner a number of primer sets.

Group IV (claims 27-31), drawn to a method of obtaining a real and a virtual mass spectrum.

Group V (claim 32), drawn to a method of determining a similarity criteria.

Group VI (claim 33), drawn to a method of generating a synthetic mass spectrum template.

Group VII (claims 34-41), drawn to a method of grouping a plurality of biological members.

The inventions listed as Groups I-VII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Each of the inventions of groups I-VII are distinct processes because each has distinct steps and produces different results, and each has its own special technical features. For group I, the special technical feature is comparing computationally a plurality of genotype sequences of a plurality of members and determining a distinguishing genotype sequence for said members. For group II, it is determining computationally a level of identification obtained from a first primer set and repeating the step with additional primer sets until said level of identification is at least equal to a desired level. For group III, it is obtaining a virtual amplicon of a portion of a member of a biological sample, comparing the virtual amplicon with a database of virtual amplicons, and repeating the steps with additional virtual amplicons until the level of identification is at or above a desired level. For group IV, it is providing a virtual sample and obtaining a real and virtual mass spectrum of the sample. For group V, it is obtaining a mass spectrum of a bioagent sample, and comparing the mass spectrum with at least a second virtual mass spectrum of the sample. For group VI, it is obtaining a mass spectrum of a primer pair amplicon and transforming the mass spectrum into a mass spectrum model. For group VII, it is obtaining at least one grouping criteria and comparing the grouping criteria of at least one member with the grouping criteria of one other member to determine an interrelatedness between the members.